



1600

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/634,109D

DATE: 03/27/2003

TIME: 12:39:13

Input Set : A:\6202NCP.txt

Output Set: N:\CRF4\03272003\I634109D.raw

4 <110> APPLICANT: Gabriel Vogeli  
 5 Linda S. Wood  
 7 <120> TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR EXPRESSED IN BRAIN  
 9 <130> FILE REFERENCE: 28341/6202NCP  
 11 <140> CURRENT APPLICATION NUMBER: US 09/634,109D  
 12 <141> CURRENT FILING DATE: 2000-08-08  
 14 <150> PRIOR APPLICATION NUMBER: US 09/377,563  
 15 <151> PRIOR FILING DATE: 2000-08-19  
 17 <160> NUMBER OF SEQ ID NOS: 14  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 948  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (1)...(945)  
 30 <400> SEQUENCE: 1  
 31 atg gga aga tgg gtg aac cag tcc tac aca gat ggc ttc ttc ctc ttg 48  
 32 Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu  
 33 1 5 10 15  
 35 ggc atc ttt tcc cac agc cag act gac ctt gtc ctc ttc tct gca gtt 96  
 36 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val  
 37 20 25 30  
 39 atg gtg gtc ttc aca gtg gcc ctc tgt ggg aat gtc ctc ctc atc ttc 144  
 40 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe  
 41 35 40 45  
 43 ctc atc tac ctg gac gct gga ctt cac acc ccc atg tac ttc ttc ctc 192  
 44 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu  
 45 50 55 60  
 47 agc cag ctc tcc ctc atg gac ctc atg ttg gtc tgt aac att gtg cca 240  
 48 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro  
 49 65 70 75 80  
 51 aag atg gca gcc aac ttc ctg tct ggc agg aag tcc atc tcc ttt gtg 288  
 52 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val  
 53 85 90 95  
 55 ggc tgt ggc ata caa att ggc ttt ttt gtc tct ctt gtg gga tct gag 336  
 56 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu  
 57 100 105 110  
 59 ggg ctc ttg ctg gga ctc atg gct tat gac cac tac gtg gcc gtt agc 384  
 60 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser  
 61 115 120 125  
 64 cac cca ctt cac tat ccc atc ctc atg aat cag agg gtc tgt ctc cag 432

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65 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
66      130      135      140
68 att act ggg agc tcc tgg gcc ttt ggg ata ata gat gga gtg att cag 480
69 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
70 145      150      155      160
72 atg gtg gca gcc atg ggc tta cct tac tgt ggc tca agg agc gtg gat 528
73 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
74      165      170      175
76 cac ttt ttc tgt gag gta caa gct tta ttg aag ctg gcc tgt gca gac 576
77 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
78      180      185      190
80 act tcc ctt ttt gac acc ctc ctc ttt gct tgc tgt gtc ttc atg ctt 624
81 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
82      195      200      205
84 ctc ctt ccc ttc tcc atc atc atg gcc tcc tat gct tgc atc cta ggg 672
85 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
86      210      215      220
88 gct gtg ctc cga ata cgc tct gct cag gcc tgg aaa aaa gcc ctg gcc 720
89 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
90 225      230      235      240
92 acc tgc tcc tcc cac cta aca gct gtc acc ctc ttc tat ggg gca gcc 768
93 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
94      245      250      255
96 atg ttc atg tac ctg agg cct agg cgc tac cgg gcc cct agc cat gac 816
97 Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
98      260      265      270
100 aag gtg gcc tct atc ttc tac aca gtc ctt act ccc atg ctg aac ccc 864
101 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
102      275      280      285
104 ctc att tac agc ttg agg aat ggg gag gtg atg ggg gca ctg agg aag 912
105 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
106      290      295      300
108 ggg ctg gac cgc tgc agg att ggc agc cag cac tga 948
109 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
110 305      310      315
113 <210> SEQ ID NO: 2
114 <211> LENGTH: 315
115 <212> TYPE: PRT
116 <213> ORGANISM: Homo sapiens
118 <400> SEQUENCE: 2
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120 1      5      10      15
122 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
123      20      25      30
126 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
127      35      40      45
129 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
130      50      55      60
132 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro

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133 65          70          75          80
135 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
136          85          90          95
138 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
139          100          105          110
141 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser
142          115          120          125
144 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
145          130          135          140
147 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
148 145          150          155          160
150 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
151          165          170          175
153 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
154          180          185          190
156 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
157          195          200          205
159 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
160          210          215          220
162 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
163 225          230          235          240
165 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
166          245          250          255
168 Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
169          260          265          270
171 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
172          275          280          285
174 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
175          290          295          300
177 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
178 305          310          315
181 <210> SEQ ID NO: 3
182 <211> LENGTH: 22
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
188 SEQUENCE
190 <400> SEQUENCE: 3
191 gcctctatct tctacacagt cc 22
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 20
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
201 SEQUENCE
203 <400> SEQUENCE: 4
204 ccaaaaccta taaaccatcc 20

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207 <210> SEQ ID NO: 5
208 <211> LENGTH: 59
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
214     SEQUENCE
216 <400> SEQUENCE: 5
217 gcactagtaa tacgactcac tatagggaga ccaccatggg aagatgggtg aaccagtcc 59
220 <210> SEQ ID NO: 6
221 <211> LENGTH: 60
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
227     SEQUENCE
229 <400> SEQUENCE: 6
230 gactggatcc cccgggcttt tttttttttt ttgcggccgc tcagtgtctgg ctgccaatcc 60
233 <210> SEQ ID NO: 7
234 <211> LENGTH: 9
235 <212> TYPE: PRT
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Description of Artificial Sequence: MAP KINASE
240     SUBSTRATE PEPTIDE
242 <400> SEQUENCE: 7
243 Ala Pro Arg Thr Pro Gly Gly Arg Arg
244   1           5
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 316
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
252 <400> SEQUENCE: 8
253 Met Asp Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
254   1           5           10           15
256 Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser
257           20           25           30
259 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
260           35           40           45
262 Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
263           50           55           60
265 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
266           65           70           75           80
268 Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
269           85           90           95
271 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
272           100          105          110
274 Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
275           115          120          125

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277 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
278      130      135      140
281 Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser
282 145      150      155      160
284 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
285      165      170      175
287 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
288      180      185      190
290 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
291      195      200      205
293 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
294      210      215      220
296 Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
297 225      230      235      240
299 Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
300      245      250      255
302 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
303      260      265      270
305 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
306      275      280      285
308 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
309      290      295      300
312 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
313 305      310      315
316 <210> SEQ ID NO: 9
317 <211> LENGTH: 223
318 <212> TYPE: PRT
319 <213> ORGANISM: Mus musculus
321 <400> SEQUENCE: 9
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323 1      5      10      15
325 Lys Met Ala Val Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Ala
326      20      25      30
328 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
329      35      40      45
331 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
332      50      55      60
334 His Pro Leu His Tyr Pro Ile Leu Met Ser Gln Lys Val Cys Leu Gln
335 65      70      75      80
337 Ile Ala Gly Ser Ser Trp Ala Phe Gly Ile Leu Asp Gly Ile Ile Gln
338      85      90      95
340 Met Val Ala Ala Met Ser Leu Pro Tyr Cys Gly Ser Arg Tyr Ile Asp
341      100      105      110
343 His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ala Asp
344      115      120      125
346 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
347      130      135      140
349 Leu Leu Pro Phe Ser Ile Ile Val Thr Ser Tyr Ala Arg Ile Leu Gly
350 145      150      155      160

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**VERIFICATION SUMMARY**

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